

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 12:13:46 ; Search time 17 seconds

(without alignments)
672.941 Million cell updates/sec

Title: US-10-015-967-2

Perfect score: 644
Sequence: 1 MKVLISLLLLPLTMSMV.....SRACQFLKQCQLRSFALPL 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR.L3:*
2: PIR.L1:*
3: PIR.L2:*
4: PIR.L4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77.5	12.0	477	2 T18801	hypothetical prote
2	77	12.0	2269	1 J01750	genome polypeptide
3	74.5	11.6	448	2 I50451	vitamin D receptor
4	73.5	11.4	70	2 A60912	vitamin D receptor
5	71.5	11.1	108	2 G84522	similar to gibber
6	71	11.0	411	2 S35333	steroid receptor p
7	71	11.0	2262	2 S16664	large protein L -
8	71	11.0	3190	2 T13828	CRB-binding prote
9	70.5	10.9	1283	2 T49804	hypothetical prote
10	70	10.9	543	2 A32693	steroid receptor p
11	70	10.9	746	2 B32693	steroid receptor p
12	70	10.9	1095	2 T24061	hypothetical prote
13	70	10.9	1620	2 T27283	hypothetical prote
14	69.5	10.8	221	2 C34768	ORF2 protein - Orf
15	69.5	10.8	575	1 THHUB	thrombomodulin pre
16	69	10.7	200	2 C83086	hypothetical prote
17	68.5	10.6	381	2 A46358	steroid/thyroid ho
18	68.5	10.6	422	2 PC4019	vitamin D receptor
19	68.5	10.6	423	2 A31761	1,25-dihydroxyvita
20	68.5	10.6	427	2 A28200	vitamin D receptor
21	68.5	10.6	427	2 S24174	vitamin D receptor
22	68.5	10.6	647	2 S36557	El protein - human
23	68.5	10.6	1006	2 S74992	hypothetical prote
24	68	10.6	283	2 S42393	G-box-binding prot
25	67	10.4	376	2 T48950	cysteine proteinase
26	67	10.4	475	2 E69643	histidine permease
27	67	10.4	1062	2 T14151	Inv protein - mous
28	67	10.4	1062	2 T30255	inversin - mouse
29	66.5	10.3	103	2 A72713	hypothetical prote

30	66.5	10.3	419	2 A57000
31	66.5	10.3	422	2 I48305
32	66.5	10.3	423	2 S02710
33	66	10.2	339	2 T36061
34	65.5	10.2	106	2 S60232
35	65.5	10.2	397	2 S20617
36	65.5	10.2	413	2 H82270
37	65.5	10.2	425	2 JC7230
38	65.5	10.2	646	2 S36586
39	65.5	10.2	706	2 JE0164
40	65	10.1	363	2 JCA748
41	65	10.1	440	2 JS0374
42	65	10.1	1797	2 A55677
43	64.5	10.0	359	2 B29960
44	64.5	10.0	622	2 I48733
45	64	9.9	227	2 I39313

ALIGNMENTS

RESULT 1

T18801 hypothetical protein ZK131.11 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000

C:Accession: T18801, T27746

R:Pericy, C.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z19024

A:Accession: T18801

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-477 <MT12>

A:Cross-references: EMBL:Z93373; PIDN: CAB07552.1; GSPDB: GN00020; CESP: ZK131.11

A:Experimental source: clone C01B9

A:Reference number: Z20413

A:Accession: T27746

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-477 <MT12>

A:Cross-references: EMBL:Z83245; PIDN: CAB05840.1; GSPDB: GN00020; CESP: ZK131.11

A:Experimental source: clone ZK131

A:Genetics:

A:Map position: 2

A:introns: 20/2; 49/2; 113/1; 169/1; 260/2; 375/3; 432/3

C:Superfamily: Caenorhabditis elegans hypothetical protein ZK131.11

Query Match

Best local similarity 12.0%; Score 77.5; DB 2; Length 477;

Matches 25; Conservative 6; Mismatches 32; Indels 9; Gaps 3;

DB 290 GGNMNSNTTFLRATRFKKITTSATLPKKNSTMDNFQSSVFEDTAHHNNMNG 349

QY 101 RACQFLKQCQL 112

DB 350 R---ILKRAPL 357

orphan receptor CO
gene CUP-TF1 prot
transcription fact
hypothetical prote
gibberellin-regula
transcription fact
hypothetical prote
vitamin D receptor
El protein - human
fizzled-6 protein
polygalacturonase
hypothetical 51.6k
laminin beta-2 cha
Balbiani ring 2 ch
protein kinase rock
zinc-finger protei

RESULT 2

J01750 genome polypeptide - simian paramyxovirus SV41 (strain Toshiba/Chanock)

N:Alternate names: RNA nucleotidyltransferase (RNA-directed); RNA replicase

C:Species: simian paramyxovirus SV41

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 11-Jun-1999

C:Accession: J01750
R:Ogawa, M.; Mutsuga, N.; Tsurudome, M.; Kawano, M.; Matsumura, H.; Kusagawa, S.; Kom

J. Gen. Virol. 73, 2743-2750, 1992
 A:Title: Nucleotide sequence analysis of the simian virus 41 gene encoding the large (L)
 A:Reference number: J01750; MUID:93019033; PMID:1328485
 A:Accession: J01750
 A:Molecule type: mRNA
 A:Residues: 1-2269 <CGA>
 A:Cross-references: EMBL:X64275; NID:g433516; PIDD:CAA45569.1; PID:g433522
 A:Gene: L
 C:Genetics:
 A:Superfamily: parainfluenza virus RNA-directed RNA polymerase
 C:Keywords: Arp; nucleotidyltransferase; RNA biosynthesis; RNA replication

Query Match 12.0%; Score 77; DB 1; Length 2269;
 Best Local Similarity 27.5%; Pred. No. 10;
 Matches 30; Conservative 12; Mismatches 31; Indels 36; Gaps 6;

13 PLMLSNVSSSLNPGVARGHNRGAS-----RRWLQ-----EGGQCE--CK 53
 422 PLSLGNMSKSL-----IEHNNSEISYEYTLRHWKELSLIEPKCFDPDGEISIFMK 477
 QY 54 DWFLAPRRKEMTVSGLPKQCPDHFKNVKKTRHQRHHRKPNKHSR 101
 DB 478 DKALAPKEDMMSV-----FRKSLIKRHRHHPMPNPFNR 514

RESULT 3
 150451
 vitamin D receptor isoform A - Japanese quail
 C:Species: Coturnix coturnix japonica (Japanese quail)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Sep-1999
 C:Accession: I50451
 R:Relation: M.A.; Prahl, J.M.; Deluca, H.F.
 Proc. Natl. Acad. Sci. U.S.A. 91, 11596-11600, 1994
 A:Title: The avian vitamin D receptors; primary structures and their origins.
 A:Reference number: I50451; MUID:95062315; PMID:7972109
 A:Accession: I50451
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-448 <EIA>
 A:Cross-references: EMBL:U12641; NID:9595500; PIDD:AAA56725.1; PID:9595501
 C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
 C:Keywords: zinc finger
 F:42-362/Domain: erba transforming protein homology <ERBA>

Query Match 11.6%; Score 74.5; DB 2; Length 448;
 Best Local Similarity 32.9%; Pred. No. 4.5;
 Matches 24; Conservative 11; Mismatches 15; Indels 23; Gaps 6;

QY 50 CE-CKDWFLAPRRKEMTVSGLPKQCPDHFKNVKKTRHQRHHRKPNKHSRACQFLK 108
 DB 61 CECKGFFRRSRKRAMFT-----CP---FSGDCKITRDNR-----RHCQACR--LK 102

QY 109 QC-----QLRSEFAL 117
 DB 103 RCVDIGMKKEFIL 115

RESULT 4
 A60912
 vitamin D receptor - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 12-Sep-1997
 C:Accession: A60912
 R:McDonnell, D.P.; Mangelsdorf, D.J.; Pike, J.W.; Haussler, M.R.; O'Malley, B.W.
 Science 235, 1214-1217, 1987
 A:Title: Molecular cloning of complementary DNA encoding the avian receptor for vitamin
 A:Reference number: A60912; MUID:87149040; PMID:3029866
 A:Accession: A60912
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-70 <MCD>
 C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
 C:Keywords: DNA binding; zinc finger

F:1-70/Domain: erba transforming protein homology (fragment) <ERBA>

Query Match 11.4%; Score 73.5; DB 2; Length 70;
 Best Local Similarity 35.5%; Pred. No. 1.2;
 Matches 22; Conservative 9; Mismatches 12; Indels 19; Gaps 5;

QY 50 CE-CKDWFLAPRRKEMTVSGLPKQCPDHFKNVKKTRHQRHHRKPNKHSRACQFLK 108
 DB 20 CECKGFFRRSRKRAMFT-----CP---FSGDCKITRDNR-----RHCQACR--LK 61

QY 109 QC 110
 DB 62 RC 63

RESULT 5
 G84522
 similar to gibberellin-regulated proteins [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 01-Mar-2002
 C:Accession: G84522
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fuji, C.Y.
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanhaken, S.E.; Umayam, L.; Tallon,
 eus, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: G84522
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-108 <STO>
 A:Cross-references: GB:AE002093; NID:g3650032; PIDD:AAC61287.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g14900
 A:Map position: 2
 C:Superfamily: gibberellin-regulated protein GASA2

Query Match 11.1%; Score 71.5; DB 2; Length 108;
 Best Local Similarity 25.9%; Pred. No. 2.7;
 Matches 29; Conservative 18; Mismatches 38; Indels 27; Gaps 7;

QY 1 MKVLISLILL-LPLMLSNVSSSLNPGVARG-----HRDRGQASRWLDGQCE-- 51
 DB 1 MKTIVSLIVLASLILSSISLASFITSDAGSGAVAPAPSKGPALEKWC---GQKCGSR 57

QY 52 CKDWFLAPRRKEMTVSGLPKQCPDHFKNVKKTRHQRHHRKPNKHSRAC 103
 DB 58 CKR---AGMKDRCLKYGICCKKDCQC-----VPSGTY-----GNKHCAC 94

RESULT 6
 S35333
 steroid receptor protein svp44 - zebra fish
 C:Species: Brachydanio rerio (zebra fish)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 24-Sep-1999
 C:Accession: S35333
 R:Eljose, A.; Normes, S.; Weber, U.; Mlodzik, M.
 EMBO J. 12, 1403-1414, 1993
 A:Title: Functional conservation of vertebrate seven-up related genes in neurogenesis
 A:Reference number: S35333; MUID:932323680; PMID:8467797
 A:Accession: S35333
 A:Molecule type: mRNA
 A:Residues: 1-411 <RJO>
 A:Cross-references: EMBL:X70299; NID:g296418; PIDD:CAA9780.1; PID:g296419
 C:Genetics:
 A:Gene: svp44
 C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
 C:Keywords: DNA binding; steroid hormone receptor; zinc finger
 F:74-320/Domain: erba transforming protein homology <ERBA>
 F:76-96/Region: zinc finger
 F:112-136/Region: zinc finger

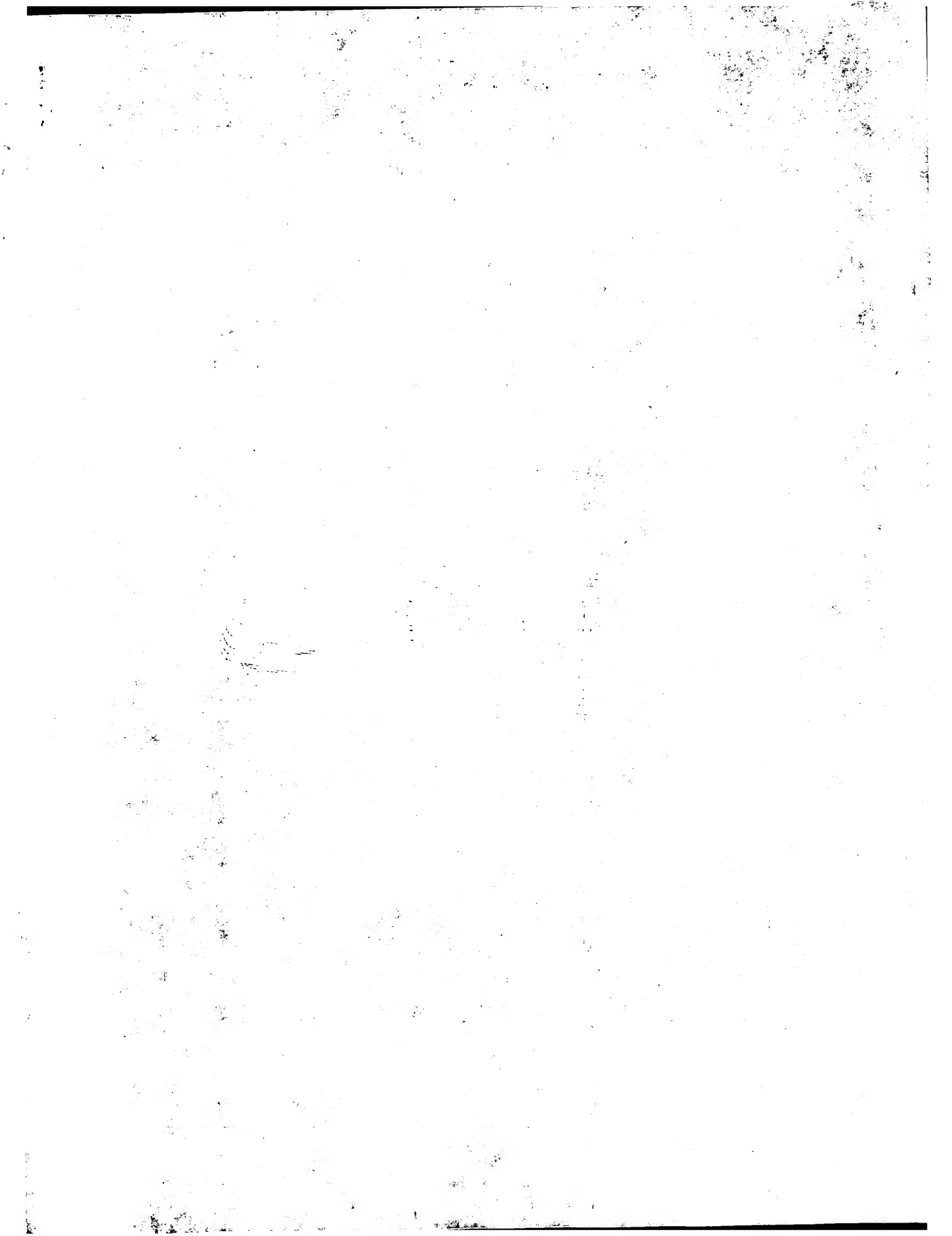
Query Match 11.0%; Score 71; DB 2; Length 411;

Proc. Natl. Acad. Sci. U.S.A. 84, 6425-6429, 1987
A:Title: Human thrombomodulin gene is intron depleted: nucleic acid sequences of the cDN
A:Reference number: A28307; MUID:87317665; PMID:2819876
A:Accession: A28307
A:Molecule type: DNA; mRNA
A:Residues: 1-472, 'A', 474-575 <JNC>
A:Cross-references: GB:J02973; NID:9339658; PIDN:AA61175.1; PID:9339659
R:Suizuki, K.; Kusumoto, H.; Deyashiki, Y.; Nishio, J.; Maruyama, I.; Yushi, M.; Kawah
EMBO J. 6, 1891-1897, 1987
A:Title: Structure and expression of human thrombomodulin, a thrombin receptor on endoth
A:Reference number: A29680; MUID:88004395; PMID:2820710
A:Accession: A29680
A:Molecule type: mRNA
A:Residues: 1-575 <SUZ>
A:Cross-references: GB:X05495; NID:937123; PIDN:CAA29045.1; PID:9736251
A:Experimental source: lung endothelium
A:Note: part of this sequence, including the amino end of the mature protein, were deter
R:Men, D.; Dittman, W.A.; Ye, R.D.; Deaven, L.L.; Majerus, P.W.; Sadler, J.E.
Biochemistry 26, 4350-4357, 1987
A:Title: Human thrombomodulin: complete cDNA sequence and chromosome localization of the
A:Reference number: A27073; MUID:88024950; PMID:2822087
A:Accession: A27073
A:Molecule type: mRNA
A:Residues: 1-472, 'A', 474-575 <MEN>
A:Cross-references: GB:M16552; NID:9339656; PIDN:AAB59508.1; PID:9339657
A:Experimental source: placenta
A:Note: parts of this sequence were determined by protein sequencing
R:Yamamoto, S.; Mitsuuchi, T.; Tamaki, T.; Ohkuchi, M.; Kimura, S.; Aoki, N.
J. Biochem. 113, 433-440, 1993
A:Title: Urinary thrombomodulin, its isolation and characterization.
A:Reference number: JX0264; MUID:93293792; PMID:8390446
A:Accession: JX0264
A:Molecule type: protein; mRNA
A:Residues: 19-472, 'A', 474-486 <YAM>
A:Experimental source: urine
A:Note: the urinary form appears to be identical with that circulating in plasma
R:Gerlitz, B.; Hassell, T.; Vlahos, C.V.; Parkinson, J.F.; Bang, N.U.; Grinnell, B.W.
Biochem. J. 295, 131-140, 1993
A:Title: Identification of the predominant glycosaminoglycan-attachment site in soluble
serine.
A:Reference number: S38954; MUID:94029900; PMID:8216207
A:Accession: S38954
A:Molecule type: protein
A:Residues: 475-491, 'X', 493-494 <GER>
A:Note: the residue designated 'X' was determined to be a Ser with covalently bound chon
R:Meininger, D.P.; Komives, E.A.
submitted to the Brookhaven Protein Data Bank, September 1995
A:Reference number: A67363; PDB:1ZAO
A:Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue
R:Tulinsky, A.; Mathews, I.I.
A:Reference number: A52804; PDB:1HLF
A:Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 426-442
R:Haral, R.; Komives, E.A.; Ni, F.
submitted to the Brookhaven Protein Data Bank, November 1995
A:Reference number: A65583; PDB:1FGD
A:Contents: annotation; conformation by (1)H-NMR, residues 427-444
R:Haral, R.; Komives, E.A.; Ni, F.
Protein Sci. 5, 195-203, 1996
A:Title: Structural resiliency of an EGF-like subdomain bound to its target protein, the
A:Reference number: A58595; MUID:96276211; PMID:8745396
A:Contents: annotation; conformation by (1)H-NMR
C:Genetics:
A:Gene: GDB:THBD
A:Cross-references: GDB:119613; OMIM:188040
A:Map position: 20p11.2-20p11.2
A:Introns: #status absent
A:Complex: homodimer, urinary form
C:Function:
A:Description: inhibits thrombin activation of fibrinogen; cofactor for thrombin activat
A:Pathway: blood coagulation moderation
A:Note: the membrane-bound form is located on the endothelium luminal surface of arterie
A:Note: thrombin complexed with the membrane-bound form is subject to endocytosis

C:Superfamily: thrombomodulin; C-type lectin homology; EGF homology
C:Keywords: anticoagulant; beta-hydroxyasparagine; beta-hydroxyaspartic acid; blood c
e protein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-575/Product: thrombomodulin, membrane-bound form #status predicted <MAT>
F:19-513/Domain: extracellular #status predicted <EXT>
F:19-486/Product: thrombomodulin, urinary form #status experimental <MAU>
F:24-167/Domain: C-type lectin homology <LCH>
F:177-199/Region: PEST sequence
F:201-233/Region: PEST sequence
F:245-280/Domain: EGF homology <EG1>
F:288-323/Domain: EGF homology <EG2>
F:329-362/Domain: EGF homology <EG3>
F:369-404/Domain: EGF homology <EG4>
F:408-439/Domain: EGF homology <EG5>
F:445-480/Domain: EGF homology <EG6>
F:485-513/Region: PEST sequence
F:517-539/Domain: transmembrane #status predicted <TMN>
F:540-575/Domain: intracellular #status predicted <INT>
F:47,115,116,382,409/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:174,225,411,504/Binding site: carbohydrate (Thr) (covalent) #status predicted
F:245-256,257-265,267-280,288-296,297-308,310-323,329-340,336-349,351-362,369-378,374
F:334,498/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:342/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental
F:490,492/Binding site: chondroitin sulfate (Ser) (covalent) #status experi

Query Match 10.8%; Score 69.5; DB 1; Length 575;
Best local similarity 23.5%; Pred. No. 19;
Matches 24; Conservative 11; Mismatches 26; Indels 41; Gaps 5;
QY 5 ISSLLLLPLMLSMWSSSLNPGVARGHNDGASRRM---IQEGGCECKKDFLRAPR 61
Db 209 VGSSAAVAPGLQDMCTAP--PCAVGHWAR-EAPGAMDCSEVNGCEHCN----- 257
QY 62 RKPMVSGPKKCP-----CDHF 80
Db 258 ----ALPGAPRCQCPAGALQADGRSCTASATGSCNDLCSEHF 295

Search completed: April 16, 2003, 12:16:36
Job time : 20 secs



```
DB    2430 QHTNCK--RRPNGCPICKQLINAC 2453

RESULT 9
T49804
hypothetical protein B1JB22_60 [Imported] - Neurospora crassa
C|Species: Neurospora crassa
C|Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
G|Accession: T49804
R|Schulte, U.; Aign, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu  
submitted to the Protein Sequence Database, May 2000
A|Reference number: Z250Z2
A|Accession: T49804
A|Status: preliminary
A|Molecule type: DNA
A|Residues: 11283 <SCH>
A|Cross-references: EMBL:AL356834; GSPDB:GN00116; NCSP:B1JB22_60
A|Experimental source: BAC clone B1JB22; strain OR74A
C|Genetics:  
A|Gene: NCSP:B1JB22_60
A|Map position: 6
A|Introns: 856/2

Query Match          10.9%   Score 70.5; DB 2; Length 1283;  
Best Local Similarity 24.5%; Pred.No. 29;  
Matches 26; Conservative 18; Mismatches 31; Indels 31; Gaps 6;
```

```
OY      33 RDRCASRRRWLOEGGECEKDMFLRAPRKRFMTVS---GLPKQCPCDHFKNVAK--T 87
        ||::||::||||| | | | | | | | :||::
Db     454 RNKKKKKRKMKEGSKSK-----LRAPESAMPVSVWGPSPSRPMLPRMOGHIRNGDV 508

OY      88 RHQRHR-----KPNNKSRAQCF-LKOCILRSFA 116
        ||::||::| | | | | | | | | | | | | | | | | |
Db     509 GHOSHNGHWMDGYVRRLMSEKLPH----QQPARLKRELALAYA 550


RESULT 10
A32693
steroid receptor protein svp 1 - fruit fly (Drosophila melanogaster)
C|Species: Drosophila melanogaster
C|Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Sep-1999
G|Accession: A32693
R|Mlodzik, M.; Hitomi, Y.; Weber, U.; Goodman, C.S.; Rubin, G.M.  
Cell 60, 211-224, 1990
A|Title: The Drosophila seven-up gene, a member of the steroid receptor gene superfam  
A|Reference number: A32693; PMID:90124631; PMID:2105166
A|Accession: A32693
A|Status: preliminary
A|Molecule type: mRNA
A|Residues: 1-543 <MKO>
A|Cross-references: GB:M2863; NID:g158518; PIDN:AAA62770.1; PID:g158519
C|Genetics:  
A|Gene: FlyBase:svp
A|Cross-references: FlyBase:FBNgn0003651
C|Superfamily: unassigned erba-related proteins; erba transforming protein homology  
C|Keywords: alternative splicing; DNA binding; steroid hormone receptor; transcriptio  
F:196-432/Doman: erba transformling protein homology <ERBA>
F:200-220/Region: zinc finger  
F:236-260/Region: zinc finger
```

```
Query Match          10.9%   Score 70; DB 2; Length 543;  
Best Local Similarity 26.7%; Pred.No. 16;  
Matches 27; Conservative 12; Mismatches 28; Indels 34; Gaps 5;
```

```
OY      21 SSSLNP-----VARGHRDGQSRRWLDEGGCECDMFLLARPFRKFMTVSG 69
        ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::
Db     183 SQSSNSGSDISKNIIECVVGDKSSKHYGQFCPEG-----CSFKFSRYRN-LITYSC 236

OY      70 LPKQCPCDHFKNVKTRHQRHRHKPNKHSBPAAQQFLKOC 110
        ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::
db     237 RGSRNCPLD-----QHNRNCOYLGR-----LKKC 260
```

RESULT 11

B32693

steroid receptor protein svp 2 - fruit fly (*Drosophila melanogaster*)C:Species: *Drosophila melanogaster*

C>Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 12-Sep-1997

C:Accession: B32693

R:Modczlik, M.; Hitomi, Y.; Weber, U.; Goodman, C.S.; Rudin, G.M.

C:Title: The *Drosophila* seven-up gene, a member of the steroid receptor gene superfamily

C:Reference number: A32693; MUID:90124631; PMID:2105166

A:Accession: B32693

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-746 <MLO>

A:Cross-references: GB:M28863; GB:M28864

C:Genetics:

A:Gene: FlyBase:FBgn0003651

A:Cross-references: FlyBase:FBgn0003651

C:Superfamily: unassigned erba-related proteins; erba transforming protein homology

C:Keywords: alternative splicing; DNA binding; steroid hormone receptor; transcription

F:198-452/Domain: erba transforming protein homology <ERBA>

F:200-220/Region: zinc finger

F:236-260/Region: zinc finger

Query Match 10.9%; Score 70; DB 2; Length 746;

Best Local Similarity 26.7%; Pred. No. 21;

Matches 27; Conservative 12; Mismatches 28; Indels 34; Gaps 5;

Oy	21	SSSLNPG-----	-VARGHRRGQASRWLQEGGECCKDWFLRPRKMTVSG	69
Db	183	SSSSNGSGIDSKONIECVCGDKSGKHGCTCEG-----	CKSPFKSRVRN-LTYSC	236

Oy	70	LKKQCCPCHEFGKGVKTRHQRHRRKPKHSRACQOFLKCC	110
Db	237	RGRNRCPID-----QHRRNQCYCR-----LKKC	260

RESULT 12

T24061

hypothetical protein R09A8.1 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T24061

R:Wilkinson, J.

Submitted to the EMBL Data Library, November 1995

A:Reference number: Z19836

A:Accession: T24061

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1095 <MLO>

A:Cross-references: EMBL:268009; PIDN:CAA92003.1; GSPDB:GN00028; CESP:R09A8.1

A:Experimental source: clone R09A8

C:Genetics:

A:Gene: CESP:R09A8.1

A:Map position: x

A:Introns: 48/2; 189/1; 285/3; 347/3; 402/3; 482/3; 543/3; 619/1; 693/1; 771/1; 835/1; 1

Query Match 10.9%; Score 70; DB 2; Length 1095;

Best Local Similarity 31.6%; Pred. No. 29;

Matches 24; Conservative 10; Mismatches 32; Indels 10; Gaps 3;

Oy	20	VSSSLNPGVARGHRRGQASRWLQEGGECCKDWFLRPRKMTVSGLPKQCCPDH	79	
Db	305	VQSSSLWGNRSTDDRNA-QRFASSTFVEECRRMQLVKKQ-----	KKEVNSDH	355

Oy	80	FKGNVKKTRHQRHRRK	95
Db	356	KKAN-RITSLEHNSR	370

RESULT 13

T27283

hypothetical protein Y64G10A.f - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T27283

R:Ainscough, R.

submitted to the EMBL Data Library, September 1999

A:Reference number: Z20336

A:Accession: T27283

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1620 <MLO>

A:Cross-references: EMBL:AL110498; NID:e1542303; PIDN:CA854471.1; CESP:Y64G10A.f

A:Experimental source: clone Y64G10A

C:Genetics:

A:Gene: CESP:Y64G10A.f

A:Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1

Query Match 10.9%; Score 70; DB 2; Length 1620;

Best Local Similarity 30.0%; Pred. No. 41;

Matches 21; Conservative 10; Mismatches 35; Indels 4; Gaps 3;

Oy	46	GGGECCKDMF-LRPRKMTVSGLPKQCCPDHFKGVKTRH--QRHRRKPKHSRA	102
Db	261	GRACCCCPGFFHLSYDRSCVDIDECANN--GCHRCENKGTCKCRBEYQLGRGRT	319

Oy	103	COOFLKCOL	112
Db	320	CEMLGGCOV	329

RESULT 14

C34768

ORF2 protein - Orf virus (strain NZ)

C:Species: Orf virus

C>Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 08-Oct-1999

C:Accession: C34768

R:Fraser, K.M.; Hill, D.F.; Mercer, A.A.; Robinson, A.J.

Virology 176, 379-389, 1990

A:Title: Sequence analysis of the inverted terminal repetition in the genome of the p

A:Reference number: A34768; MUID:90266454; PMID:2129563

A:Accession: C34768

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-221 <FRA>

A:Cross-references: GB:M30023; EMBL:M37623; NID:g332561; PIDN:AAA46789.1; PID:g332565

Query Match 10.8%; Score 69.5; DB 2; Length 221;

Best Local Similarity 29.2%; Pred. No. 8.1;

Matches 33; Conservative 8; Mismatches 37; Indels 35; Gaps 6;

Oy	26	PGVARGHRRGQASRWLQEGGECCKDWFLRPRKMTVSGLPK-----	QCP	76
Db	83	PAARAGARRGCCARRRAGGGWP---RWRPRAARRG-----	SGPPARAPAAALAPDQAP	135

Oy	77	CDHFKGVKTR-----	HR--HRRKPKHSRACQOFLKCOL	114
Db	136	---RSRVKIDRLAVETLPPQPTPTPLPRAKRRSQOACTPRACGSAKS	184	

RESULT 15

THHDB

thrombomodulin precursor [validated] - human

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1988 #sequence_revision 12-May-1995 #text_change 15-Sep-2000

C:Accession: A41442; A28307; A29680; A27073; JX0264; S38954

C:Title: T.; Shiojiri, S.; Ito, H.; Yamamoto, S.; Kusumoto, H.; Degashiki, Y.; Maruy

J.; Blochem, 103, 281-285, 1988

A:Title: Gene structure of human thrombomodulin, a cofactor for thrombin-catalyzed ac

A:Reference number: A41442; MUID:88227901; PMID:2836377

A:Accession: A41442

A:Molecule type: DNA

A:Residues: 1-575 <SHI>

A:Cross-references: DDBJ:DD00210; NID:g220126; PIDN:BA000149.1; PID:g220127

R:Jackman, R.W.; Beeler, D.L.; Fritze, L.; Soff, G.; Rosenberg, R.D.